```
FILE 'REGISTRY' ENTERED AT 10:40:12 ON 26 SEP 2005

=> S RECOMBINASE/CN
L1            1 RECOMBINASE/CN

=> D

L1   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2005 ACS on STN
RN   308064-57-5  REGISTRY *
* Use of this CAS Registry Number alone as a search term in other STN files may
  result in incomplete search results.  For additional information, enter HELP
  RN* at an online arrow prompt (=>).
ED   Entered STN:  12 Dec 2000
CN   Enzymes, DNA-recombining  (CA INDEX NAME)
OTHER NAMES:
CN   Deoxyribonucleic recombinase
CN   DNA recombinase
CN   DNA recombinases
CN   DNA-recombining enzymes
CN   Endoenzymes, DNA-recombining
CN   Recombinase
CN   Recombinases
MF   Unspecified
CI   MAN, CTS
SR   CA

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***


=> S NUCLEASE/CN
L2            1 NUCLEASE/CN

=> D

L2   ANSWER 1 OF 1  REGISTRY  COPYRIGHT 2005 ACS on STN
RN   9026-81-7  REGISTRY
ED   Entered STN:  16 Nov 1984
CN   Nuclease (9CI)  (CA INDEX NAME)
OTHER NAMES:
CN   Nucleic acid hydrolase
MF   Unspecified
CI   MAN
LC   STN Files:   ADISNEWS, AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA,
       CAPLUS, CASREACT, CEN, CHEMCATS, CIN, CSCHEM, EMBASE, IFICDB, IFIPAT,
       IFIUDB, NAPRALERT, PROMT, TOXCENTER, USPAT2, USPATFULL

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
            2554 REFERENCES IN FILE CA (1907 TO DATE)
              66 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
            2556 REFERENCES IN FILE CAPLUS (1907 TO DATE)


=> S ALKALINE NUCLEASE/CN
L3            0 ALKALINE NUCLEASE/CN

=> S DNA BINDING PROTEIN/CN
L4            0 DNA BINDING PROTEIN/CN

=> S DNA BINDING POLYPEPTIDE/CN
L5            0 DNA BINDING POLYPEPTIDE/CN

FILE 'CAPLUS' ENTERED AT 10:41:32 ON 26 SEP 2005
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=> S RECOMBINASE;S NUCLEASE;S L1 OR L6;S L2 OR L7
          3184 RECOMBINASE
           574 RECOMBINASES
L6        3400 RECOMBINASE
                 (RECOMBINASE OR RECOMBINASES)


         20606 NUCLEASE
          6247 NUCLEASES
L7       24750 NUCLEASE
                 (NUCLEASE OR NUCLEASES)


             0 L1
L8        3400 L1 OR L6


          2556 L2
L9       24828 L2 OR L7

=> S L1
L10          0 L1

=> S HERPES SIMPLEX;S UL12 OR (UL(W)12);S ICP8 OR (ICP(W)8)
         24159 HERPES
         24282 SIMPLEX
            97 SIMPLEXES
         24339 SIMPLEX
                 (SIMPLEX OR SIMPLEXES)
L11      18559 HERPES SIMPLEX
                 (HERPES(W)SIMPLEX)


            48 UL12
          8633 UL
           116 ULS
          8741 UL
                 (UL OR ULS)
       1342918 12
             5 UL(W)12
L12         51 UL12 OR (UL(W)12)


           219 ICP8
         22442 ICP
           353 ICPS
         22595 ICP
                 (ICP OR ICPS)
       2624217 8
            15 ICP(W)8
L13        227 ICP8 OR (ICP(W)8)

=> S L11 AND L12 AND L13
L14          5 L11 AND L12 AND L13

=> D 1-5 CBIB ABS

L14  ANSWER 1 OF 5  CAPLUS  COPYRIGHT 2005 ACS on STN
2005:617071   Document No. 143:244793  Herpes simplex virus
     type 1 single-strand DNA binding protein ICP8 enhances the
     nuclease activity of the UL12 alkaline nuclease by increasing
     its processivity.  Reuven, Nina Bache; Weller, Sandra K. (Department of
     Molecular, Microbial, and Structural Biology, University of Connecticut
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Health Center, Farmington, CT, 06030-3205, USA). Journal of Virology, 79(14), 9356-9358 (English) 2005. CODEN: JOVIAM. ISSN: 0022-538X. Publisher: American Society for Microbiology.

AB UL12 is a 5'- to 3'-exonuclease encoded by herpes simplex virus type 1 (HSV-1) which degrades single- and double-stranded DNA. UL12 and the single-strand DNA binding protein ICP8 mediate a strand exchange reaction. We found that ICP8 inhibited UL12 digestion of single-stranded DNA but stimulated digestion of double-stranded DNA threefold. The stimulatory effect of ICP8 was independent of a strand exchange reaction; furthermore, the effect was specific to ICP8, as it could not be reproduced by Escherichia coli single-stranded DNA binding protein. The effect of ICP8 on the rate of UL12 double-stranded DNA digestion is attributable to an increase in processivity in the presence of ICP8.

L14 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

2004:673325 Document No. 141:327554 Catalysis of Strand Exchange by the HSV-1 UL12 and ICP8 Proteins: Potent ICP8 Recombinase Activity is Revealed upon Resection of dsDNA Substrate by Nuclease. Reuven, Nina B.; Willcox, Smaranda; Griffith, Jack D.; Weller, Sandra K. (Department of Molecular, Microbial, and Structural Biology, University of Connecticut Health Center, Farmington, CT, 06030-3205, USA). Journal of Molecular Biology, 342(1), 57-71 (English) 2004. CODEN: JMOBAK. ISSN: 0022-2836. Publisher: Elsevier.

AB The replication of herpes simplex virus type 1 (HSV-1) is associated with a high degree of homologous recombination, which is likely to be mediated, in part, by HSV-1-encoded proteins. We have previously shown that the HSV-1 encoded ICP8 protein and alkaline nuclease UL12 are capable of catalyzing an in vitro strand-exchange reaction. Here, we show, by electron microscopy, that the products of the strand exchange reaction between linear double-stranded DNA and circular single-stranded DNA consist of the expected joint mol. forms: sigma, alpha, and gapped circles. Other exonucleases, such as lambda Red α, which, like UL12, digests 5'-3', as well as Escherichia coli exonuclease III (ExoIII), which digests 3'-5', could substitute for UL12 in the strand exchange reaction by providing a resected DNA end. ICP8 generated the same intermediates and strand exchange products when the double-stranded DNA substrate was preresected by any of the nucleases. Using substrates with large regions of non-homol. we found that pairing by ICP8 could be initiated from the middle of a DNA mol. and did not require a homologous end. In this reaction, the resection of a DNA end by the nuclease is required to reveal homologous sequences capable of being paired by ICP8. This study further illustrates the complexity of the multi-functional ICP8 protein.

L14 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

2004:589029 Document No. 141:102234 Herpes simplex virus 1 recombinase comprising a purified or isolated alk. nuclease UL12 and a single stranded DNA binding protein ICP8. Weller, Sandra; Myers, Richard S.; Reuven, Nina Bacher (USA). U.S. Pat. Appl. Publ. US 2004141994 A1 20040722, 31 pp. (English). CODEN: USXXCO. APPLICATION: US 2003-656868 20030904. PRIORITY: US 2002-PV408092 20020904.

AB A Herpes simplex virus (HSV) recombinase comprises a purified or isolated alkaline nuclease and a single stranded DNA binding protein. In HSV-1, the alkaline nuclease is the UL12 protein and the single stranded DNA binding protein is the ICP8 protein. The HSV recombinase can be purified from an in vitro expression system or can be expressed in an appropriate vector or vectors wherein the DNAs encoding the polypeptides are operatively linked to expression control sequences. Methods of use of the HSV recombinase include cloning, treating cells and organisms, and producing transgenic animals. The HSV recombinase can be in the form of a kit useful for cloning.

L14 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

2004:346110 Document No. 141:49571 The UL12.5 gene product of

herpes simplex virus type 1 exhibits nuclease and strand exchange activities but does not localize to the nucleus. Reuven, Nina Bacher; Antoku, Susumu; Weller, Sandra K. (Department of Molecular, Microbial, University of Connecticut Health Center, Farmington, CT, 06030-3205, USA). Journal of Virology, 78(9), 4599-4608 (English) 2004. CODEN: JOVIAM. ISSN: 0022-538X. Publisher: American Society for Microbiology.

AB The herpes simplex virus type 1 (HSV-1) alkaline nuclease, encoded by the UL12 gene, plays an important role in HSV-1 replication, as a null mutant of UL12 displays a severe growth defect. Although the precise in vivo role of UL12 has not yet been determined, several in vitro activities have been identified for the protein, including endo- and exonuclease activities, interaction with the HSV-1 single-stranded DNA binding protein ICP8, and an ability to promote strand exchange in conjunction with ICP8. In this study, we examined a naturally occurring N-terminally truncated version of UL12 called UL12.5. Previous studies showing that UL12.5 exhibits nuclease activity but is unable to complement a UL12 null virus posed a dilemma and suggested that UL12 .5 may lack a critical activity possessed by the full-length protein, UL12. We constructed a recombinant baculovirus capable of expressing UL12.5 and purified soluble UL12.5 from infected insect cells. The purified UL12.5 exhibited both endo- and exonuclease activities but was less active than UL12. Like UL12, UL12.5 could mediate strand exchange with ICP8 and could also be coimmunopptd. with ICP8. The primary difference between the two proteins was in their intracellular localization, with UL12 localizing to the nucleus and UL12.5 remaining in the cytoplasm. We mapped a nuclear localization signal to the N terminus of UL12, the domain absent from UL12.5. In addition, when UL12.5 was overexpressed so that some of the enzyme leaked into the nucleus, it was able to partially complement the UL12 null mutant.

L14 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

2003:489987 Document No. 139:144854 The herpes simplex virus type 1 alkaline nuclease and single-stranded DNA binding protein mediate strand exchange in vitro. Reuven, Nina Bacher; Staire, Amy E.; Myers, Richard S.; Weller, Sandra K. (Department of Microbiology, University of Connecticut Health Center, Farmington, CT, 06030-3205, USA). Journal of Virology, 77(13), 7425-7433 (English) 2003. CODEN: JOVIAM. ISSN: 0022-538X. Publisher: American Society for Microbiology.

AB The replication of herpes simplex virus type 1 (HSV-1) DNA is associated with a high degree of homologous recombination. While cellular enzymes may take part in mediating this recombination, we present evidence for an HSV-1-encoded recombinase activity. HSV-1 alkaline nuclease, encoded by the UL12 gene, is a 5'→3' exonuclease that shares homol. with Redα, commonly known as λ exonuclease, an exonuclease required for homologous recombination by bacteriophage lambda. The HSV-1 single-stranded DNA binding protein ICP8 is an essential protein for HSV DNA replication and possesses single-stranded DNA annealing activities like the Redβ synaptase component of the phage lambda recombinase. Here we show that UL12 and ICP8 work together to effect strand exchange much like the Red system of lambda. Purified UL12 protein and ICP8 mediated the complete exchange between a 7.25-kb M13mp18 linear double-stranded DNA mol. and circular single-stranded M13 DNA, forming a gapped circle and a displaced strand as final products. The optimal conditions for strand exchange were 1 mM MgCl2, 40 mM NaCl, and pH 7.5. Stoichiometric amts. of ICP8 were required, and strand exchange did not depend on the nature of the double-stranded end. Nuclease-defective UL12 could not support this reaction. These data suggest that diverse DNA viruses appear to utilize an evolutionarily conserved recombination mechanism.

=> S SPODOPTERA
L15 6182 SPODOPTERA

=> S L15 AND L11
L16 30 L15 AND L11

=> S L16 AND (L12,L13)
L17 0 L16 AND ((L12 OR L13))

=> S L16 NOT L14
L18 30 L16 NOT L14

=> D 1-30 CBIB ABS

L18 ANSWER 1 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
2004:165602 Document No. 140:319738 Immunogenicity and efficacy of baculovirus derived glycoprotein D of herpes simplex virus type-1 in mice. Soleimanjahi, H.; Roostaee, M. H.; Rassaee, M. J.; Mahboodi, F.; Bamdad, T. (Virology Dept., Faculty of Medical Sciences, Tarbiat Modarres University, Tehran, Iran). Archives of Razi Institute, 55, 19-28 (English) 2003. CODEN: ARIRCA. Publisher: Razi Vaccine & Serum Research Institute.

AB The recombinant glycoprotein D (gD) of herpes simplex virus type-1 (HSV-1) in baculovirus expression system was produced. Spodoptera Frugiperda cell, clone 9 (Sf9) was cultured in modified Grace's medium and inoculated with 5-7 multiplicity of infection of HSV-1 recombinant baculovirus carrying gD gene. Inoculated cells were harvested 96h post-inoculation and treated with 3-[(3-cholamidopropyl)dimethylammoni o]-1-propanesulfonate (CHAPS) and phenylmethylsulfonyl fluoride (PMSF) and sonicated at 20 kHz for 5 times. A Western blot was developed and applied to detect the prepared protein. Three groups of BALB/c mice each of 7 mice were inoculated with the recombinant gD, sublethal dose of challenge virus (104.5 TCID50) and PBS resp. All inoculated mice were challenged with 10MLD50 (106.5 TCID50) of the wild HSV-1. All mice who had received the recombinant gD survived while 14.3% and 71.5% of mice inoculated resp. with either sublethal dose of the virus or PBS died.

L18 ANSWER 2 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
2001:580627 Document No. 136:227498 Cloning, sequencing and baculovirus-based expression of fusion-glycoprotein D gene of herpes simplex virus type 1 (F). Uh, Hong Sun; Choi, Jin Hee; Byun, Si Myung; Kim, Soo Young; Lee, Hyung Hoan (Department of Biological Sciences, Konkuk University, Seoul, 143-701, S. Korea). Journal of Biochemistry and Molecular Biology, 34(4), 371-378 (English) 2001. CODEN: JBMBE5. ISSN: 1225-8687. Publisher: Springer-Verlag Singapore Pte. Ltd..

AB The Glycoprotein D (gD) gene of the HSV-1 strain F was cloned, sequenced, recombinated into the HcNPV (Hyphantria cunea nuclear polyhedrosis virus) expression vector and expressed in insect cells. The gD gene was located in the 6.43 kb BamHI fragment of the strain F. The open reading frame (ORF) of the gD gene was 1,185 bp and codes 394 amino acid residues. Recombinant baculoviruses, GD-HcNPVs, expressing the gD protein were constructed. Spodoptera frugiperda cells, infected with the recombinant virus, synthesized a matured gX-gD fusion protein with an approx. mol. weight of 54 kDa and secreted the gD proteins into the culture media by an immunopptn. assay. The fusion gD protein was localized on the membrane of the insect cells, seen by using an immunofluorescence assay. The deduced amino acid sequence presents addnl. characteristics compatible with the structure of a viral glycoprotein: signal peptide, putative glycosylation sites and a long C-terminal transmembrane sequence. These results indicate the utility of the HcNPV-insect cell system for producing and characterizing eukaryotic proteins.

L18 ANSWER 3 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
2000:872205 Document No. 134:142517 High level production of glycoprotein H of HSV-1 (F) using HcNPV vector system. Kang, Hyun; Cha, Soung Chul; Han, You Jin; Park, In Ho; Lee, Min Jung; Byun, Si Myung; Lee, Hyung Hoan (Department of Biological Science & Institute for Genetic Engineering, Konkuk University, Seoul, 143-701, S. Korea). Journal of Biochemistry and

Molecular Biology, 33(6), 483-492 (English) 2000. CODEN: JBMBE5. ISSN: 1225-8687. Publisher: Springer-Verlag Singapore Pte. Ltd..

AB The Herpes simplex virus type 1 (HSV-1) strain F glycoprotein H (gH) gene in the pHLB-4 plasmid was recombinated into a baculovirus expression vector (lacZ-HcNPV) to construct a recombinant virus GH-HcNPV expressing gH. The sequences of gH and its expression were analyzed. The gH gene was located in the 6.41 kb BglII fragment. The open reading frame (ORF) of the gH gene was 2,517 bp and codes 838 amino acid residues. Insect cells infected with this recombinant virus synthesized a high level of the matured and gX-gH fusion protein with approx. 112 kDa. The fusion gH protein was localized on the membrane of the insect cells as seen by using immunofluorescence assay and accumulated in the cultured media by the SDS-PAGE and immunopptn. assays. The amino acid sequence presents addnl. characteristics compatible with the structure of a viral glycoprotein: signal peptide, putative glycosylation sites and a long C-terminal transmembrane sequence. Antibodies raised in mice to this recombinant protein recognized viral gH and neutralized the infectivity of HSV-1 in vitro. These results demonstrate that it is possible to produce a mature protein by gene transfer in eukaryotic cells, and indicate the utility of the HcNPV-insect cell system for producing and characterizing eukaryotic proteins. Furthermore, the neutralizing antibodies would appear to protect mice against HSV; accordingly, this particular recombinant protein may be useful in the development of a subunit vaccine.

L18 ANSWER 4 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN

2000:569496 Document No. 133:349200 Expression of the HSV-1 (F) glycoprotein B gene in insect cells infected by HcNPV recombinant. Cha, Soung Chul; Kang, Hyun; Lee, Sook Yeon; Park, Gap Ju; Lee, Hyung Hoan (Department of Biology, Konkuk University, Seoul, 143-701, S. Korea). Journal of Microbiology and Biotechnology, 10(3), 355-362 (English) 2000. CODEN: JOMBES. ISSN: 1017-7825. Publisher: Korean Society for Applied Microbiology.

AB The Herpes simplex virus type 1 (HSV-1) glycoprotein B (gB) gene in the pHLA-21 plasmid was inserted into a baculovirus (Hyphantria cunea nuclear polyhedrosis virus) expression vector (lacZ-HcNPV) to construct a recombinant virus gB-HcNPV expressing gB. Spodoptera frugiperda cells infected with this recombinant virus synthesized and processed gB of approx. 120 kDa, which cross-reacted with the monoclonal antibody to gB. The recombinant gB was identified on the membrane of the insect cells using an immunofluorescence assay. Antibodies to this recombinant raised in mice recognized the viral gB and neutralized the infectivity of the HSV-1 in vitro. These results show that the gB gene has the potential to be expressed in insect cells. They also demonstrate that it is possible to produce a mature protein by gene transfer in eukaryotic cells, and indicate the utility of the lacZ-HcNPV-insect cell system for producing and characterizing eukaryotic proteins. Furthermore, the neutralizing antibodies would appear to protect mice against HSV. Accordingly, this particular recombinant protein may be useful in the development of a subunit vaccine.

L18 ANSWER 5 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN

2000:44732 Document No. 133:69547 Constructions of a transfer vector containing the gX signal sequence of Pseudorabies virus and a recombinant baculovirus. Lee, Hyung Hoan; Kang, Hyun; Kim, Jung Woo; Hong, Seung Kuk; Kang, Bong Joo; Song, Jae Young (Department of Biology and Institute for Genetic Engineering, Konkuk University, Seoul, 143-701, S. Korea). Journal of Microbiology and Biotechnology, 9(5), 541-547 (English) 1999. CODEN: JOMBES. ISSN: 1017-7825. Publisher: Korean Society for Applied Microbiology.

AB Constructions of a transfer vector and a recombinant baculovirus using the thymidine kinase gene of the Herpes simplex virus type 1 strain F (HSV-1) were carried out. Newly cloned transfer vector, pHcgXIIIB, was constructed by insertion of the glycoprotein gX gene signal peptide sequence of Pseudorabies virus into the baculovirus vector pHcEV-IV. The gX sequence was inserted just downstream from the promoter for the polyhedrin gene of the Hyphantria cunea

nuclear polyhedrosis virus (HcNPV). HSV-1 thymidine kinase (tk) gene (1.131 kb) was used as a candidate gene for transferring into the baculovirus expression system. The tk gene was inserted into a BamHI site downstream from the gX sequence-promoter for the polyhedrin gene in the pHcgXIIIB transfer vector and was transferred into the infectious lacZ-HcNPV expression vector. Recombinant virus was isolated and was named gX-TK-HcNPV. The recombinant virus produced a 45 kDa gX-TK fusion protein in Spodoptera frugiperda cells, which was confirmed by Western blot anal. Microscopic examination of gX-TK-HcNPV-infected cells revealed normal multiplication. Fluorescent antibody staining indicated that the gX-TK fusion protein was present in the cytoplasm. These results indicated that the transfer vector successfully transferred the gX-tk gene into the baculovirus expression system.

L18 ANSWER 6 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN

1999:28941 Document No. 130:247579 The US5 open reading frame of herpes simplex virus type 1 does encode a glycoprotein (gJ). Ghiasi, Homayon; Nesburn, Anthony B.; Cai, Steve; Wechsler, Steven L. (Ophthalmology Research, Cedars-Sinai Medical Center Research Institute, Los Angeles, CA, 90048, USA). Intervirology, 41(2-3), 91-97 (English) 1998. CODEN: IVRYAK. ISSN: 0300-5526. Publisher: S. Karger AG.

AB Based on sequence anal., the protein encoded by the US5 open reading frame (ORF) of herpes simplex virus type 1 (HSV-1) was predicted to contain an N-glycosylation site and was given the designation of glycoprotein J (gJ). However, the US5 gene product has not been identified and the identity of gJ as a glycoprotein has not been confirmed. We have cloned and expressed the DNA encoding the complete sequence of the US5 ORF, using a baculovirus expression system. Western blotting, using polyclonal antibody raised against synthetic US5 peptides, revealed two major baculovirus-US5-expressed protein bands with apparent mol. wts. of 16-17 and 10 kD. The recombinant US5 was found on the membrane of Spodoptera frugiperda cells and was susceptible to tunicamycin, endoglycosidase H, glycosidase F and partially resistant to endoglycosidase F. Vaccination of mice with baculovirus-expressed US5 did not induce a neutralizing antibody to HSV-1 or provide protection against lethal HSV-1 challenge. However, serum from these vaccinated mice was able to recognize US5 in purified HSV-1 virions by Western blot analyses and on the surface of HSV-1-infected cells by immunofluorescence. These findings establish that US5 does encode a glycoprotein and confirm the appropriateness of naming the US5 gene product gJ.

L18 ANSWER 7 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN

1999:25388 Document No. 130:195466 Expression and cellular distribution of baculovirus-expressed bovine herpesvirus 1 (BHV-1) glycoprotein D (gD) sequences. Abdelmagid, O. Y.; Mansour, M. M.; Okwumabua, O.; Van Drunen Littel-Van Den Hurk, S. (Department of Pathobiology, School of Veterinary Medicine, Tuskegee University, Tuskegee, AL, USA). Archives of Virology, 143(11), 2173-2187 (English) 1998. CODEN: ARVIDF. ISSN: 0304-8608. Publisher: Springer-Verlag Wien.

AB Glycoprotein D (gD) of bovine herpesvirus 1 (BHV-1), a homolog of herpes simplex virus gD, represents a major component of the viral envelope and is a dominant immunogen. To study the antigenic properties of the different regions of gD, we have expressed the full-length gD encoding gene and overlapping fragments spanning various regions of the gD open reading frame in a baculovirus (Autographa californica nuclear polyhedrosis virus) - insect cell (Spodoptera frugiperda, SF-9) system. Maximum levels of expression for all proteins were obtained 48 to 72 h post infection of SF-9 cells by recombinant viruses. Full-length and truncated recombinant gD proteins reacted specifically with anti-gD monospecific serum as determined by immunopptn. and immunoblotting, indicating that the proteins retained their antigenicity. However, based on the reactivity with a panel of gD-specific monoclonal antibodies (Mabs), the full-length recombinant gD lacked proper expression for two highly neutralizing linear epitopes identified by Mabs R54 and 9D6. The rest of the epitopes appeared to be

preserved and antigenically unaltered. Immunofluorescence studies of recombinant baculovirus infected SF-9 cells using gD monospecific serum, revealed no direct correlation between cellular localization of the expressed proteins and their amino acid sequences.

L18 ANSWER 8 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1998:810169 Document No. 130:192612 Characterization of the acidic domain of the IE1 regulatory protein from Orgyia pseudotsugata multicapsid nucleopolyhedrovirus. Forsythe, Ian J.; Shippam, Cynthia E.; Willis, Leslie G.; Stewart, Sandra; Grigliatti, Tom; Theilmann, David A. (Department of Zoology, University of British Columbia, Vancouver, BC, V6T 1Z4, Can.). Virology, 252(1), 65-81 (English) 1998. CODEN: VIRLAX. ISSN: 0042-6822. Publisher: Academic Press.

AB This study presents a detailed anal. of the acidic N-terminal region of the Orgyia pseudotsugata multicapsid nucleopolyhedrovirus (OpMNPV) transactivator IE1. The N-terminal region of IE1 is rich in acidic amino acids and has been hypothesized to be an acidic activation domain. Removal of the N-terminal 126 amino acids containing the acidic domain of IE1 resulted in complete loss of transactivation activity, indicating that this region is essential for transactivation. The OpMNPV acidic domain was replaced with the archetype acidic activation domain from VP16 and the acid-rich region of Autographa californica multicapsid NPV (AcMNPV) IE1. These chimeric constructs were fully capable of transactivation in transient assays. The chimeric OpMNPV IE1s containing the herpes simplex virus VP16 and AcMNPV IE1 acidic activation domains consistently transactivated a reporter gene to higher levels than the OpMNPV IE1 acidic activation domain. Transactivation by the chimeric constructs is enhanced synergistically when cotransfected with IE2 into Lymantria dispar and Spodoptera frugiperda cells. Both N- to C-terminal and C- to N-terminal deletions of the OpMNPV acidic activation domain were constructed to define functional domains within the OpMNPV IE1 acidic activation domain. At least two potential activation domains were identified. Within each of these domains, two core regions at amino acids 28-43 and amino acids 113-124 were identified that were similar to core regions of VP16 and GAL4, which contain predominately acidic and bulky hydrophobic amino acids. (c) 1998 Academic Press.

L18 ANSWER 9 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1997:725129 Document No. 128:12598 Production of recombinant herpes simplex virus protease in 10-L stirred vessels using a baculovirus-insect cell expression system. Schwartz, J. L.; Ferrari, E. B.; Terracciano, J.; Troyanovich, J.; Gunnarsson, I.; Wright-Minogue, J.; Chen, J. W.; Kwong, A. D. (Department of Microbial Products-Fermentation, Kenilworth, NJ, 07033-0539, USA). Journal of Industrial Microbiology & Biotechnology, 19(2), 87-91 (English) 1997. CODEN: JIMBFL. ISSN: 1367-5435. Publisher: Stockton.

AB A gene expression system using recombinant Autographa californica nuclear polyhedrosis virus (baculovirus) and Sf-9 cells has been scaled up to the 10-L tank level and shown to be capable of producing herpes simplex virus (HSV) protease in serum-free media. High densities of Spodoptera frugiperda (Sf-9) cells were achieved by modifying two 10-L Biolafitte fermenters specifically for insect cell growth. The existing Rushton impellers were replaced by marine impellers to reduce shear and the aeration system was modified to allow external addition of air/O2 mixts. at low flow rates through either the sparge line or into the head space of the fermenter. To inoculate the tanks, Sf-9 cells were adapted to grow to high cell densities (6-10+106 cells ml-1) in shake flasks in serum-free media. With these procedures, cell densities of 5+106 cells ml-1 were routinely achieved in the 10-L tanks. These cells were readily infected with recombinant baculovirus expressing the 247-amino acid catalytic domain of the HSV-1 strain 17 protease UL26 gene as a glutathione-S-transferase (GST) fusion protein (GST-247). Three days after infection at a multiplicity of infection (MOI) of 3 pfu cell-1, the GST-247 fusion protein was purified from a cytoplasmic lysate by Glutathione Sepharose 4-B affinity chromatog. with reproducible yields

of 11-38 mg L-1 of recombinant protein and ≥ 90% purity. Maximum production of this protein was observed at a cell d. of 5.0+106 cells ml-1.

L18 ANSWER 10 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1997:627483 Document No. 127:303999 Herpes simplex virus 1 α regulatory protein ICP0 interacts with and stabilizes the cell cycle regulator cyclin D3. Kawaguchi, Yasushi; Van Sant, Charles; Roizman, Bernard (The Marjorie B. Kovler Viral Oncology Laboratories, The University of Chicago, Chicago, IL, 60637, USA). Journal of Virology, 71(10), 7328-7336 (English) 1997. CODEN: JOVIAM. ISSN: 0022-538X. Publisher: American Society for Microbiology.

AB The herpes simplex virus 1 (HSV-1) infected-cell protein 0 (ICP0) has the characteristics of a promiscuous transactivator of genes introduced into cells by infection or transfection. To identify cellular proteins inter-acting with ICP0, the authors used a domain of exon II of ICP0 that is known to be crucial for regulatory function of the protein as bait in the yeast two-hybrid screen. The results were as follows. A cDNA in a pos. yeast colony was found to encode cyclin D3, a cell cycle regulator of G1 phase. A purified chimeric protein consisting of glutathione S-transferase (GST) fused to cyclin D3 specifically formed complexes with ICP0 contained in HSV-1-infected cell lysate. To enhance the expression of cyclin D3, the gene was inserted into the viral genome and overexpressed in infected cells. The overexpressed cyclin D3 colocalized with ICP0 in nuclear structures characteristic of ND10 and which earlier have been reported to contain ICP0. The accumulation of cyclin D3 protein in Vero cells infected with an α0 deletion mutant was reduced relative to that of cells infected with wild-type virus or a recombinant virus in which the deleted α0 sequences were restored. Lysates of Spodoptera frugiperda Sf9 cells doubly infected with baculoviruses genetically engineered to express cyclin D3 and cyclin-dependent kinase 4 (CDK4) phosphorylated GST fused to retinoblastoma protein (GST-pRb) but did not phosphorylate the GST-α020-241 or GST-α0543-768 fusion protein or immunopptd. ICP0 proteins. Moreover, the chimeric GST-ICP0exon II protein shown to bind cyclin D3 had no effect on the activity of the kinase on GST-pRb when added to mixts. of lysates of Sf9 cells which coexpressed cyclin D3 and CDK4. These results indicate that ICP0 interacts with, colocalizes with, and stabilizes the cyclin D3 cell cycle regulator and does not affect its interaction with the cyclin-dependent kinase.

L18 ANSWER 11 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1995:847772 Document No. 123:283209 Preparation of monoclonal antibodies against Marek's disease virus serotype 1 glycoprotein D expressed by a recombinant baculovirus. Ono, Mitsuru; Jang, Hyung-Kwan; Maeda, Ken; Kawaguchi, Yasushi; Tohya, Yukinobu; Niikura, Masahiro; Mikami, Takeshi (Department of Veterinary Microbiology, Faculty of Agriculture, The University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo, 113, Japan). Virus Research, 38(2-3), 219-30 (English) 1995. CODEN: VIREDF. ISSN: 0168-1702. Publisher: Elsevier.

AB A recombinant baculovirus, the genome of which contains DNA encoding Marek's disease virus serotype 1 (MDV1) homolog of glycoprotein D (gD) of herpes simplex virus under the polyhedrin promoter was constructed and designated rAcMDV1gD. Five monoclonal antibodies (MAbs) which recognize the MDV1 homolog of gD (MDV1 gD) in Spodoptera frugiperda cells infected with rAcMDV1gD were prepared The MAbs reacted with proteins ranging from 52 to 49 kDa in rAcMDV1gD-infected cell lysates by immunoblot anal. These mol. wts. were coincident with mol. wts. predicted from the open reading frame of MDV1 gD. By ELISA additivity test, the 5 MAbs were divided into 3 groups which seemed to recognize 3 different epitopes. In addition, all of the 5 MAbs were reactive with chick embryo fibroblasts (CEFs) expressing MDV1 gD. The MAbs are considered to be useful to study the role of MDV1 gD in MDV1 infection.

L18 ANSWER 12 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1995:319826 Document No. 122:98808 Cloning and expression of human β2-microglobulin cDNA and the construction of fusion proteins between antigenic epitopes and β2-microglobulin. Edwards, Richard Mark; Hunter, Michael George (British Bio-Technology Ltd., UK). PCT Int. Appl. WO 9424290 A1 19941027, 30 pp. DESIGNATED STATES: W: AU, BR, CA, CN, CZ, DE, FI, GB, HU, JP, KR, NO, NZ, PL, RU, UA, US; RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1994-GB755 19940408. PRIORITY: GB 1993-7371 19930408.

AB A method is described for the cloning and expression of human β2-microglobulin (B2M) cDNA in vector host cells which allows the construction of B2M fusion proteins with antigenic sequences from various etiol. agents or tumors. Preferred antigenic sequences are derived from the third variable domain (V3 loop) of an envelope protein of a lentivirus. These fusion proteins can be used as prophylactic or immunotherapeutic vaccines to induce neutralizing antibody responses. Thus, B2M cDNA was inserted into the pHILD1 expression vector for expression in the Pichia pastoris system. The expression vector includes an AOX promoter sequence and an α-factor or Pho1 leader sequence to obtain secretion of the fusion protein from the yeast cells. Within the Pichia pastoris expression system, the B2M gene was fused at its 5' end to the Sendai virus epitope (FAPGNYPAL-GGGGG, where the pentaglycine is a short linker) or to the influenza A virus nucleoprotein epitope (GILGFVFTL-GGGGGGSSS). Production levels from strains with the α-factor leader sequence were .apprx.150 mg/L. The hybrid Sendai-B2M product was shown to induce Sendai nucleoprotein-specific cytotoxic T-lymphocytes.

L18 ANSWER 13 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1995:154369 Document No. 122:79112 Self-assembling protein particles presenting foreign epitopes on their surfaces. Adams, Sally Elizabeth; Burns, Robert Nigel; Richardson, Simon Mark Harold (British Bio-Technology Ltd., UK). PCT Int. Appl. WO 9414969 A1 19940707, 43 pp. DESIGNATED STATES: W: AU, CA, CZ, DE, FI, GB, HU, JP, KR, NO, NZ, RU, UA, US; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1993-GB2656 19931224. PRIORITY: GB 1992-27068 19921229.

AB Fusion proteins of the yeast retrotransposon Ty p1 protein and an antigenic peptide that self-assemble into particles presenting the epitope on the outside are prepared for use in vaccines. This is achieved by substituting the exposed immunodominant epitope of Ty p1 with the foreign peptide. The epitopes of the p1 protein were identified by standard methods of epitope scanning and three peptides were identified and those in the N-terminal region were found to be exposed on the surface of the protein. The TyA gene encoding the protein was manipulated to introduce convenient NheI sites in the epitope coding regions and the protein encoded by expression of these genes continued to self-associate A series of analogs with peptides from the V3 loop of gp120 of HIV-1 inserted at the epitope sites were prepared by expression of the gene in yeast and tested for their response to anti-gp120 antisera. These proteins self-assembled. The fusion proteins reacted with antisera to the p1 protein and to the V3 epitope; different antisera responded to the V3 epitope in different positions.

L18 ANSWER 14 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1994:290982 Document No. 120:290982 Assembly of herpes simplex virus (HSV) intermediate capsids in insect cells infected with recombinant baculoviruses expressing HSV capsid proteins. Thomsen, Darrell R.; Roof, Lori L.; Homa, Fred L. (Upjohn Co., Kalamazoo, MI, 49001, USA). Journal of Virology, 68(4), 2442-57 (English) 1994. CODEN: JOVIAM. ISSN: 0022-538X.

AB The capsid of herpes simplex virus type 1 (HSV-1) is composed of seven proteins, VP5, VP19C, VP21, VP22a, VP23, VP24, and VP26, which are the products of six HSV-1 genes. Recombinant baculoviruses were used to express the six capsid genes

(UL18, UL19, UL26, UL26.5, UL35, and UL38) in insect cells. All constructs expressed the appropriate-size HSV proteins, and insect cells infected with a mixture of the six recombinant baculoviruses contained large nos. of HSV-like capsids. Capsids were purified by sucrose gradient centrifugation, and electron microscopy showed that the capsids made in Sf9 cells had the same size and appearance as authentic HSV B capsids. Sodium dodecyl sulfate-polyacrylamide gel electrophoresis anal. demonstrated that the protein composition of these capsids was nearly identical to that of B capsids isolated from HSV-infected Vero cells. Electron microscopy of thin sections clearly demonstrated that the capsids made in insect cells contained the inner electron-translucent core associated with HSV B capsids. In infections in which single capsid genes were left out, it was found that the UL18 (VP23), UL19 (VP5), UL38 (VP19C), and either the UL26 (VP21 and VP24) or the UL26.5 (VP22a) genes were required for assembly of 100-nm capsids. VP22a was shown to form the inner core of the B capsid, since in infections in which the UL26.5 gene was omitted the 100-nm capsids, that formed lacked the inner core. The UL35 (VP26) gene was not required for assembly of 100-nm capsids, although assembly of B capsids was more efficient when it was present. These and other observations indicate that (i) the products of the UL18, UL19, UL35, and UL38 genes self-assemble into structures that form the outer surface (icosahedral shell) of the capsid, (ii) the products of the UL26 and/or UL26.5 genes are required (as scaffolds) for assembly of 100-nm capsids, and (iii) the interaction of the outer surface of the capsid with the scaffolding proteins requires the product of the UL18 gene (VP23).

L18 ANSWER 15 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1994:290981 Document No. 120:290981 Characterization of baculovirus-expressed herpes simplex virus type 1 glycoprotein K.
Ghiasi, Homayon; Slanina, Susan; Nesburn, Anthony B.; Wechsler, Steven L. (Res. Inst., Cedars-Sinai Med. Cent., Los Angeles, CA, 90048, USA).
Journal of Virology, 68(4), 2347-54 (English) 1994. CODEN: JOVIAM. ISSN: 0022-538X.

AB The DNA region encoding the complete herpes simplex virus type 1 (HSV-1) glycoprotein K (gK) was inserted into a baculovirus transfer vector, and recombinant viruses expressing gK were isolated. Four gK-related recombinant baculovirus-expressed peptides of 29, 35, 38, and 40 kDa were detected with polyclonal antibody to gK. The 35-, 38-, and 40-kDa species were susceptible to tunicamycin treatment, suggesting that they were glycosylated. The 38- and 40-kDa species corresponded to partially glycosylated precursor gK (pgK) and mature gK, resp. The 29-kDa peptide probably represented a cleaved, unglycosylated peptide. The 35-kDa peptide probably represented a cleaved, glycosylated peptide that may be a precursor to pgK. Indirect immunofluorescence with polyclonal antibody to gK peptides indicated that the recombinant baculovirus-expressed gK was abundant on the surface of the insect cells in which it was expressed. Mice vaccinated with the baculovirus-expressed gK produced very low levels (<1:10) of HSV-1 neutralizing antibody. Nonetheless, these mice were partially protected from lethal challenge with HSV-1 (75% survival). This protection was significant ($P = 0.02$). Despite some protection against death, gK-vaccinated mice showed no protection against the establishment of latency. Surprisingly, gK-vaccinated mice that were challenged ocularly with a stromal disease-producing strain of HSV-1 had significantly higher levels of ocular disease (herpes stromal keratitis) than did mock-vaccinated mice. In summary, this is the first report to show that vaccination with HSV-1 gK can provide protection against lethal HSV-1 challenge and that vaccination with an HSV-1 glycoprotein can significantly increase the severity of HSV-1-induced ocular disease.

L18 ANSWER 16 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1994:158700 Document No. 120:158700 Manufacture of herpes simplex virus type I glycoprotein I for use in treatment of infection. Nesburn, Anthony B.; Wechsler, Steven L.; Ghiasi, Homayon (Cedars-Sinai Medical Center, USA). Can. Pat. Appl. CA 2090303 AA 19930919, 25 pp. (English). CODEN: CPXXEB. APPLICATION: CA 1993-2090303

19930224. PRIORITY: US 1992-852999 19920318.

AB Herpes Simplex virus type 1 (HSV-1) glycoprotein I (gI) is manufactured in a baculovirus system using Sf9 cells for use in immunotherapy of HSV infections. The transfer of a cloned glycoprotein gI gene into an Autographa californica nuclear polyhedrosis virus (AcNPV) expression vector was achieved by standard methods and expressed in Sf9 cells. The protein was manufactured as a doublet of 52 and 56 kDa, with both bands reacting to a monoclonal antibody to gI. When cells were cultured in the presence of tunicamycin both members of the doublet had lower mol. wts.; glycosidation was also labile to digestion with Endo-H indicating the presence of mannoses and N-glycosidation. The protein was transported to the cell surface. Mice immunized with whole cells containing gI showed 90% survival after challenge with 2+106 pfu of HSV-I three weeks after immunization; control mice showed 60% mortality. The immunized mice had a neutralization titer of 167 (+complement) or 91 (-complement).

L18 ANSWER 17 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN

1994:126330 Document No. 120:126330 High-level expression and purification of secreted forms of herpes simplex virus type 1 glycoprotein gD synthesized by baculovirus-infected insect cells. Sisk, William P.; Bradley, Jodi D.; Leipold, Robert J.; Stoltzfus, Angeline M.; Ponce de Leon, Manuel; Hilf, Megan; Peng, Charline; Cohen, Gary H.; Eisenberg, Roselyn J. (Exp. Stn., DuPont Merck Pharm. Co., Wilmington, DE, 19880-0400, USA). Journal of Virology, 68(2), 766-75 (English) 1994. CODEN: JOVIAM. ISSN: 0022-538X.

AB Two forms of herpes simplex virus glycoprotein gD were recombined into Autographa californica nuclear polyhedrosis virus (baculovirus) and expressed in infected Spodoptera frugiperda (Sf9) cells. Each protein was truncated at residue 306 of mature gD. One form, gD-1(306t), contains the coding sequence of Patton strain herpes simplex virus type 1 gD; the other, gD-1(QAAt), contains three mutations which eliminate all signals for addition of N-linked oligosaccharides. Prior to recombination, each gene was cloned into the baculovirus transfer vector pVT-Bac, which permits insertion of the gene minus its natural signal peptide in frame with the signal peptide of honeybee melittin. As in the case with many other baculovirus transfer vectors, pVT-Bac also contains the promoter for the baculovirus polyhedrin gene and flanking sequences to permit recombination into the polyhedrin site of baculovirus. Each gD gene was engineered to contain codons for five addnl. histidine residues following histidine at residue 306, to facilitate purification of the secreted protein on nickel-containing resins. Both forms of gD-1 were abundantly expressed and secreted from infected Sf9 cells, reaching a maximum at 96 h postinfection for gD-1(306t) and 72 h postinfection for gD-1(QAAt). Secretion of the latter protein was less efficient than gD-1(306t), possibly because of the absence of N-linked oligosaccharides from gD-1(QAAt). Purification of the two proteins by a combination of immunoaffinity chromatog., nickel-agarose chromatog., and gel filtration yielded products that were >99% pure, with excellent recovery. The authors are able to obtain 20 mg of purified gD-1(306t) and 1 to 5 mg of purified gD-1(QAAt) per L of infected insect cells grown in suspension. Both proteins reacted with monoclonal antibodies to discontinuous epitopes, indicating that they retain native structure. Use of this system for gD expression makes crystallization trials feasible.

L18 ANSWER 18 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN

1994:105148 Document No. 120:105148 Manufacture of herpes simplex virus type 1 glycoprotein E in a baculovirus system for immunotherapy of viral infection. Nesburn, Anthony B.; Wechsler, Steven L.; Ghiasi, Homayon (Cedars-Sinai Medical Center, USA). Can. Pat. Appl. CA 2090295 AA 19930804, 29 pp. (English). CODEN: CPXXEB. APPLICATION: CA 1993-2090295 19930224. PRIORITY: US 1992-829947 19920203; US 1992-845920 19920304.

AB Glycoprotein E (gE) of herpes simplex virus I is manufactured in insect cell culture using a baculovirus expression vector for vaccines. A recombinant

Autographa californica nuclear polyhedrosis virus carrying the gE gene was constructed by standard in vivo recombination. A protein of the expected mol. weight that cross-reacted with a monoclonal antibody to gE was obtained from cell lysates; the protein was glycosidated in the host cells and transported to the cell surface. Mice inoculated with cell lysates produced neutralizing antibody to HSV-1 and these lysates could also induce delayed-type hypersensitivity. Innoculated mice showed resistance to challenge with live HSV-1 at a level comparable to that shown by inoculation with the KOS strain of HSV-1 (≥95% survival).

L18 ANSWER 19 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN

1993:76974 Document No. 118:76974 Stimulation of thymidine kinase activity in baculovirus-infected cells is not due to a virus-coded enzyme. Wang, X.; Xie, W.; Long, Q.; He, D.; Lin, G.; Pang, Y.; Pu, Z. (Inst. Entomol., Zhongshan Univ., Canton, Peop. Rep. China). Archives of Virology, 127(1-4), 315-19 (English) 1992. CODEN: ARVIDF. ISSN: 0304-8608.

AB A polyhedrin-pos. recombinant Autographa californica nuclear polyhedrosis virus (AcNPV) carrying a herpes simplex virus thymidine kinase gene under the control of the Syn XIV promoter, a fusion of synthetic and linker-modified polyhedrin promoters, was constructed. When this recombinant baculovirus was used to infect a variant of Spodoptera frugiperda cells deficient in thymidine kinase (TK-), a high level of TK activity was detected. These results, in conjunction with the demonstration that AcNPV could replicate in TK- S. frugiperda cells and no TK activity was found throughout infection, imply that the wild type virus-stimulated TK activity observed in S. frugiperda (TK+) cells is not contributed by a virus-coded enzyme.

L18 ANSWER 20 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN

1992:508015 Document No. 117:108015 Physical and functional interaction of human cytomegalovirus DNA polymerase and its accessory protein (ICP36) expressed in insect cells. Ertl, P. F.; Powell, K. L. (Dep. Mol. Sci., Wellcome Res. Lab., Beckenham/Kent, BR3 3BS, UK). Journal of Virology, 66(7), 4126-33 (English) 1992. CODEN: JOVIAM. ISSN: 0022-538X.

AB Expression of the human cytomegalovirus (HCMV) (AD169) DNA polymerase gene under the control of the polyhedrin promoter of Autographa californica nuclear polyhedrosis virus in Spodoptera frugiperda (Sf9) cells has provided a source of highly active CMV DNA polymerase. In exts. from CMV-infected cells, the CMV DNA polymerase is found strongly associated with an addnl. polypeptide, ICP36. This protein has been identified as the CMV homolog of the herpes simplex virus type 1 UL42 gene product and may have a similar function. When HCMV DNA polymerase and ICP36 were expressed in the same system, they interacted to form a stable complex. Moreover, ICP36 functions to stimulate the DNA polymerase activity in a template-dependent manner. The authors compared the activity of the recombinant DNA polymerase in the presence and absence of ICP36 on a number of DNA templates and measured the effect of the polymerase inhibitors phosphonoformic acid and acyclovir triphosphate.

L18 ANSWER 21 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN

1992:464272 Document No. 117:64272 Recombinant baculovirus encoding glycoprotein gIII of swine herpes virus I Yamagata-S81 strain. Inumaru, Shigeki; Yamada, Toshiharu (Norinsuisansho Kachiku Eisei Shikenjocho, Japan). Jpn. Kokai Tokkyo Koho JP 04099485 A2 19920331 Heisei, 7 pp. (Japanese). CODEN: JKXXAF. APPLICATION: JP 1990-213727 19900814.

AB Recombinant baculovirus encoding glycoprotein gIII of swine herpes virus I Yamagata-S81 strain is prepared for use as a vaccine. The gene for glycoprotein gIII recovered from plasmid pG3S was used to prepare plasmid pAcPRG3 which was co-transfected into the SF21AE cells of Spodoptera frugiperda with the DNA of Autographa californica nuclear polyhedrosis virus. A recombinant virus AcPRG3 was obtained. The SF21AE cells infected with the recombinant virus AcPRG3 produced glycosylated gIII.

L18 ANSWER 22 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1992:124677 Document No. 116:124677 Herpes simplex virus type 1 origin-dependent DNA replication in insect cells using recombinant baculoviruses. Stow, Nigel D. (Med. Res. Counc. Virol. Unit, Inst. Virol., Glasgow, G11 5JR, UK). Journal of General Virology, 73(2), 313-21 (English) 1992. CODEN: JGVIAY. ISSN: 0022-1317.

AB The min. set of 7 herpes simplex virus type 1 (HSV-1) genes required for viral origin-dependent DNA synthesis was previously identified using a transient replication assay in a mammalian cell line permissive for HSV-1 growth. Recombinant baculoviruses were constructed which efficiently express the products of each of these 7 genes in infected Spodoptera frugiperda (Sf) insect cells. When Sf cells were transfected with a plasmid containing a functional HSV-1 origin of replication and subsequently superinfected with a mixture of these 7 viruses, the input plasmid was amplified. This amplification exhibited properties characteristic of genuine HSV-1 DNA replication: all 7 HSV-1 replication gene products were required, replicated DNA was detected as concatemers, and mutated origins were impaired to similar extents in insect cells and cells permissive for HSV-1 replication. These results demonstrate that the HSV-1 proteins expressed in Sf cells are fully competent for viral DNA synthesis and indicate that any host function essential in mammalian cells must also be present in the infected insect cells. This system also provides a convenient method by which mutated replication proteins can be screened for function and produced in amts. sufficient for biochem. studies. Using this approach, it is shown that the ability of the UL9 protein to bind to the viral origins of replication is not sufficient for it to facilitate DNA synthesis.

L18 ANSWER 23 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1992:122203 Document No. 116:122203 Immunoselection of recombinant baculoviruses expressing high levels of biologically active herpes simplex virus type 1 glycoprotein D. Ghiasi, Homayon; Nesburn, A. B.; Kaiwar, Ravi; Wechsler, S. L. (Cedars-Sinai Med. Cent., Los Angeles, CA, 90048, USA). Archives of Virology, 121(1-4), 163-78 (English) 1991. CODEN: ARVIDF. ISSN: 0304-8608.

AB The DNA sequence encoding the complete herpes simplex virus type 1 (HSV-1) glycoprotein D (gD) was inserted into a baculovirus transfer vector under control of the polyhedrin gene promoter of the baculovirus Autographa california nuclear polyhedrosis virus (AcNPV). After co-transfection of Spodoptera frugiperda (Sf9) insect cells with wild-type AcNPV DNA and the recombinant transfer vector DNA, polyhedrin-neg. recombinants that expressed high levels of HSV-1 gD were isolated using immunoaffinity selection with antibody coated magnetic particles followed by plaque purification These recombinant baculoviruses expressed a protein that was slightly smaller than virion HSV-1 gD made in Vero cells. This recombinant protein was expressed at high levels. The expressed protein was glycosylated, was found on the membrane of Sf9 cells, and reacted with gD specific antibodies. Antibodies raised in mice to the recombinant gD neutralized Hsv-1 as measured by plaque reduction assays. Mice inoculated with the recombinant baculovirus were completely protected from lethal challenge with HSV-1.

L18 ANSWER 24 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1992:81680 Document No. 116:81680 Expression of herpes simplex virus type 1 glycoprotein B in insect cells. Initial analysis of its biochemical and immunological properties. Ghiasi, Homayon; Kaiwar, Ravi; Nesburn, Anthony B.; Wechsler, Steven L. (Cedars-Sinai Med. Cent., Los Angeles, CA, 90048, USA). Virus Research, 22(1), 25-39 (English) 1992. CODEN: VIREDF. ISSN: 0168-1702.

AB A recombinant baculovirus (vAc-gB1) was constructed which expresses the glycoprotein B (gB) gene of herpes simplex virus type 1 (HSV-1). When Sf9 cells were infected with these recombinant viruses, a protein that was close in size to authentic HSV-1 gB was detected by gB polyclonal antibody. The recombinant gB

was found on the membrane of Sf9 cells and was susceptible to tunicamycin, glycosidase F, and partially susceptible to Endo-H. Antibodies raised in mice to this recombinant recognized viral gB and neutralized the infectivity of HSV-1 in vitro. Mice inoculated with the recombinant gB were protected from lethal challenge with HSV-1.

L18 ANSWER 25 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1992:38307 Document No. 116:38307 Lepidoperan cell variants resistant to 5-bromodeoxyuridine and their use for transfection of the HSV-TK gene. Xie, Weidong; He, Daifen; Wang, Xunzhang; Long, Qingxin; Pu, Zhelong (Res. Inst. Entomol., Zhongshan Univ., Guangzhou, 510275, Peop. Rep. China). Journal of Cell Science, 100(1), 243-7 (English) 1991. CODEN: JNCSAI. ISSN: 0021-9533.
AB Following mutagenesis of cultured lepidopteran cells (Spodoptera frugiperda) by ethylmethanesulfonate, 3 variants resistant to 5-bromodeoxyuridine (BrdUrd) were isolated. These clones were 100-200-fold more resistant to BrdUrd than the parental cells and were shown to be deficient in thymidine kinase (TK). The drug-resistant phenotype was stable for up to 3 yr of culture under nonselective conditions. It was also found that the S. frugiperda cell line was highly resistant to aminopterin. A selective medium was formulated and used to select herpes simplex virus thymidine kinase (HSV-TK) transfectants from the TK-deficient cells.

L18 ANSWER 26 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1990:212858 Document No. 112:212858 Enzymic activities of overexpressed herpes simplex virus DNA polymerase purified from recombinant baculovirus-infected insect cells. Marcy, Alice I.; Olivo, Paul D.; Challberg, Mark D.; Coen, Donald M. (Dep. Biol. Chem. Mol. Pharmacol., Harvard Med. Sch., Boston, MA, 02115, USA). Nucleic Acids Research, 18(5), 1207-15 (English) 1990. CODEN: NARHAD. ISSN: 0305-1048.
AB The biochem. characterization of the herpes simplex virus (HSV) DNA polymerase, a model DNA polymerase and an important target for antiviral drugs, has been limited by a lack of pure enzyme in sufficient quantity. To overcome this limitation, the HSV DNA polymerase gene was introduced into the baculovirus, Autographa californica nuclear polyhedrosis virus, under the control of the polyhedrin promoter to give rise to a recombinant baculovirus, BP58. BP58-infected Spodoptera frugiperda insect cells expressed a polypeptide that was indistinguishable from authentic polymerase by several immunol. and biochem. properties, at levels .apprx.10-fold higher per infected cell than found in HSV-infected Vero cells. The DNA polymerase was purified to apparent homogeneity from BP58-infected insect cells. Using activated DNA as primer-template, the purified enzyme exhibited specific activity similar to that of enzyme isolated from HSV-infected Vero cells, indicating that addnl. polymerase-associated proteins from HSV-infected cells are not critical for activity with this primer-template. 3'-5'-Exonuclease activity copurified with the BP58-expressed HSV DNA polymerase, demonstrating that this activity is intrinsic to the polymerase polypeptide. The purified enzyme also exhibited RNase H activity. The recombinant baculovirus should permit detailed biochem. and biophys. studies of this enzyme.

L18 ANSWER 27 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1990:211935 Document No. 112:211935 Overexpression and assembly of the herpes simplex virus type 1 helicase-primase in insect cells [Erratum to document cited in CA111(23):210078t]. Dodson, Mark S.; Crute, James J.; Bruckner, Robert C.; Lehman, I. R. (Dep. Biochem., Stanford Univ., Stanford, CA, 94305-5307, USA). Journal of Biological Chemistry, 265(8), 4769 (English) 1990. CODEN: JBCHA3. ISSN: 0021-9258.
AB A corrected Table I has been provided. The error was not reflected in the abstract or the index entries.

L18 ANSWER 28 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1989:610078 Document No. 111:210078 Overexpression and assembly of the herpes simplex virus type 1 helicase-primase in insect cells. Dodson, Mark S.; Crute, James J.; Bruckner, Robert C.; Lehman, I. R. (Dep. Biochem., Stanford Univ., Stanford, CA, 94305-5307, USA). Journal of Biological Chemistry, 264(35), 20835-8 (English) 1989. CODEN: JBCHA3. ISSN: 0021-9258.

AB Herpes simplex virus type 1 (HSV-1) encodes a helicase-primase that consists of three polypeptides encoded by the UL5, UL8, and UL52 genes. To obtain sufficient quantities of the enzyme for study, the three genes were overexpressed using the baculovirus expression system. It was found that the fully active enzyme can be assembled in vivo by triply infecting Spodoptera frugiperda SF9 cells with a baculovirus recombinant for each gene. The recombinant enzyme which was purified to near homogeneity from the insect cells has a mol. weight of 270,000 and is composed of the three polypeptides encoded by the UL5, UL8, and UL52 genes. The enzyme possesses DNA-dependent ATPase, DNA-dependent GTPase, DNA helicase, and DNA primase activities that are essentially identical to the enzyme isolated from HSV-1-infected cells.

L18 ANSWER 29 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1989:150673 Document No. 110:150673 An efficient procedure for the isolation of recombinant baculovirus. Pen, Jan; Welling, Gjalt W.; Welling-Wester, Sytske (Lab. Med. Microbiol., Rijksuniv. Groningen, Groningen, 9713 EZ, Neth.). Nucleic Acids Research, 17(1), 451 (English) 1989. CODEN: NARHAD. ISSN: 0305-1048.

AB The isolation of recombinant baculovirus was performed by cotransfection of Spodoptera frugiperda cells with the transfer vector pAcgD267 (containing a glycoprotein D DNA fragment of herpes simplex virus type 1) and Autographa californica nuclear polyhedrosis virus DNA and then harvesting extracellular virus and determining titer 1 wk later. Recombinant virus was detected by hybridization with a glycoprotein D probe, restriction enzyme anal., and Southern hybridization. Advantages of this procedure are discussed.

L18 ANSWER 30 OF 30 CAPLUS COPYRIGHT 2005 ACS on STN
1988:543489 Document No. 109:143489 Herpes simplex virus DNA replication: the UL9 gene encodes an origin-binding protein. Olivo, Paul D.; Nelson, Nancy J.; Challberg, Mark D. (Lab. Viral Dis., Natl. Inst. Allergy Infect. Dis., Bethesda, MD, 20892, USA). Proceedings of the National Academy of Sciences of the United States of America, 85(15), 5414-18 (English) 1988. CODEN: PNASA6. ISSN: 0027-8424.

AB Herpes simplex virus 1 contains 7 genes that are necessary and sufficient for origin-dependent DNA synthesis in cultured cells. The product of one of these genes, UL9, was expressed in insect cells by using a baculovirus expression vector. The apparent size of the UL9 protein, both in insect cells and in herpes simplex virus-infected Vero cells, is 82,000 daltons. An immunoassay for protein-DNA interaction demonstrated that UL9 protein binds specifically to the herpes simplex virus origins of DNA replication, oriS and oriL. DNase I footprint anal. showed that the UL9 protein interacts with 2 related sites on oriS, located on each arm of a nearly perfect palindrome. This data strongly suggests that the origin-binding activity described previously by P. Elias et al. (1986) is the product of the UL9 gene.

=> S L12 AND L13
L19 5 L12 AND L13

=> S L19 NOT L14
L20 0 L19 NOT L14

=> S DNA BINDING
735127 DNA

```
         18011 DNAS
        737931 DNA
                  (DNA OR DNAS)
        886902 BINDING
          1946 BINDINGS
        887453 BINDING
                  (BINDING OR BINDINGS)
L21      51463 DNA BINDING
                  (DNA(W)BINDING)

=> S DNA(W)BINDING(W)(PROTEIN OR POLYPEPTIDE)
        735127 DNA
         18011 DNAS
        737931 DNA
                  (DNA OR DNAS)
        886902 BINDING
          1946 BINDINGS
        887453 BINDING
                  (BINDING OR BINDINGS)
       1787431 PROTEIN
       1244990 PROTEINS
       2077762 PROTEIN
                  (PROTEIN OR PROTEINS)
         99122 POLYPEPTIDE
         57489 POLYPEPTIDES
        135259 POLYPEPTIDE
                  (POLYPEPTIDE OR POLYPEPTIDES)
L22      10743 DNA(W)BINDING(W)(PROTEIN OR POLYPEPTIDE)

=> S L9 AND L22
L23        314 L9 AND L22

=> S L23 AND L8
L24          5 L23 AND L8

=> S L24 NOT L14
L25          3 L24 NOT L14

=> D 1-3 CBIB ABS

L25  ANSWER 1 OF 3  CAPLUS  COPYRIGHT 2005 ACS on STN
2005:955842  The PD-(D/E)XK superfamily revisited: Identification of new
     members among proteins involved in DNA metabolism and functional
     predictions for domains of (hitherto) unknown function.  Kosinski, Jan;
     Feder, Marcin; Bujnicki, Janusz M. (Laboratory of Bioinformatics and
     Protein Engineering, International Institute of Molecular and Cell
     Biology, Warsaw, PL-02-109, Pol.).  BMC Bioinformatics, 6, No pp. given
     (English) 2005.  CODEN: BBMIC4.  ISSN: 1471-2105.  URL:
     http://www.biomedcentral.com/content/pdf/1471-2105-6-172.pdf  Publisher:
     BioMed Central Ltd..
AB   The PD-(D/E)XK nuclease superfamily, initially identified in type II restriction
     endonucleases and later in many enzymes involved in DNA recombination and repair,
     is one of the most challenging targets for protein sequence anal. and structure
     prediction.  Typically, the sequence similarity between these proteins is so low,
     that most of the relationships between known members of the PD-(D/E)XK
     superfamily were identified only after the corresponding structures were
     determined exptl. Thus, it is tempting to speculate that among the
     uncharacterized protein families, there are potential nucleases that remain to be
     discovered, but their identification requires more sensitive tools than
     traditional PSI-BLAST searches.  The low degree of amino acid conservation
     hampers the possibility of identification of new members of the PD-(D/E)XK
     superfamily based solely on sequence comparisons to known members. Therefore, the
     authors used a recently developed method HHsearch for sensitive detection of
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remote similarities between protein families represented as profile Hidden Markov Models enhanced by secondary structure. The authors carried out a comparison of known families of PD-(D/E)XK nucleases to the database comprising the COG and PFAM profiles corresponding to both functionally characterized as well as uncharacterized protein families to detect significant similarities. The initial candidates for new nucleases were subsequently verified by sequence-structure threading, comparative modeling, and identification of potential active site residues. In this article, the authors report identification of the PD-(D/E)XK nuclease domain in numerous proteins implicated in interactions with DNA but with unknown structure and mechanism of action (such as putative recombinase RmuC, DNA competence factor CoiA, a DNA-binding protein SfsA, a large human protein predicted to be a DNA repair enzyme, predicted archaeal transcription regulators, and the head completion protein of phage T4) and in proteins for which no function was assigned to date (such as YhcG, various phage proteins, novel candidates for restriction enzymes). The results contributes to the reduction of "white spaces" on the sequence-structure-function map of the protein universe and will help to jump-start the exptl. characterization of new nucleases, of which many may be of importance for the complete understanding of mechanisms that govern the evolution and stability of the genome.

L25 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

2001:634531 Document No. 136:258038 Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021. Capela, Delphine; Barloy-Hubler, Frederique; Gouzy, Jerome; Bothe, Gordana; Ampe, Frederic; Batut, Jacques; Boistard, Pierre; Becker, Anke; Boutry, Marc; Cadieu, Edouard; Dreano, Stephane; Gloux, Stephanie; Godrie, Therese; Goffeau, Andre; Kahn, Daniel; Kiss, Erno; Lelaure, Valerie; Masuy, David; Pohl, Thomas; Portetelle, Daniel; Puhler, Alfred; Purnelle, Benedicte; Ramsperger, Ulf; Renard, Clotilde; Thebault, Patricia; Vandenbol, Micheline; Weidner, Stefan; Galibert, Francis (Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, Unite Mixte de Recherche (UMR) 215 Centre National de la Recherche Scientifique (CNRS), Institut National de la Recherche Agronomique, Chemin, Tolosan, F-31326, Fr.). Proceedings of the National Academy of Sciences of the United States of America, 98(17), 9877-9882 (English) 2001. CODEN: PNASA6. ISSN: 0027-8424. Publisher: National Academy of Sciences.

AB Sinorhizobium meliloti is an α-proteobacterium that forms agronomically important N2-fixing root nodules in legumes. We report here the complete sequence of the largest constituent of its genome, a 62.7% GC-rich 3654,135-bp circular chromosome. Annotation allowed assignment of a function to 59% of the 3341 predicted protein-coding ORFs, the rest exhibiting partial, weak, or no similarity with any known sequence. Unexpectedly, the level of reiteration within this replicon is low, with only two genes duplicated with more than 90% nucleotide sequence identity, transposon elements accounting for 2.2% of the sequence, and a few hundred short repeated palindromic motifs (RIME1, RIME2, and C) widespread over the chromosome. Three regions with a significantly lower GC content are most likely of external origin. Detailed annotation revealed that this replicon contains all housekeeping genes except two essential genes that are located on pSymB. Amino acid/peptide transport and degradation and sugar metabolism appear as two major features of the S. meliloti chromosome. The presence in this replicon of a large number of nucleotide cyclases with a peculiar structure, as well as of genes homologous to virulence determinants of animal and plant pathogens, opens perspectives in the study of this bacterium both as a free-living soil microorganism and as a plant symbiont.

L25 ANSWER 3 OF 3 CAPLUS COPYRIGHT 2005 ACS on STN

1996:610212 Document No. 125:267510 Methods and kits for fractionating a population of DNA molecules based on the presence or absence of a base-pair mismatch utilizing mismatch repair systems. Modrich, Paul L.; Su, Shin-san; Au, Karin G.; Lahue, Robert S.; Cooper, Deani L.; Worth, Jr Leroy (Duke University, USA). U.S. US 5556750 A 19960917, 31 pp.,

Cont.-in-part of U.S. Ser. No. 2,529,abandoned. (English). CODEN: USXXAM. APPLICATION: US 1993-145837 19931101. PRIORITY: US 1989-350983 19890512; US 1993-2529 19930111.

AB A method for eliminating DNA mols. containing ≥1 base pair mismatches from a population of heterohybrid duplex DNA mols. formed by base pairing of single-stranded DNA mols. obtained from a first source and a second source comprises 4 steps. The first is digesting genomic DNA from the first and second sources with a restriction endonuclease. The second is methylating the DNA from one of the sources. The third is denaturing the DNA from both sources and mixing the DNA in the presence of a recombinase, proteins of a mismatch repair system which modulate the recombinase, single-strand binding protein and ATP, such that DNA duplexes form in homologous regions of the DNA mols. from the first and second sources and the presence of a base pair mismatch results in regions that remain single-stranded. The fourth is removing mols. that contain said single-stranded regions from the DNA population. A modification of this method, comprising use of dideoxynucleotide triphosphates may be used for genomic mismatch scanning. Another modification for fractionating DNA populations comprises used of biotinylated NTP's in the above system and removal of DNA containing the biotinylated nucleotide through use of avidin. Expts. with E. coli proteins indicated that DNA mismatch correction required MutH, MutL, MutS, MutU (DNA helicase II), single-strand DNA binding protein, DNA polymerase III, exonuclease I, DNA ligase, and ATP. Further expts. involved examination of DNA sites involved in repair by the above system and strand-specific repair directed by DNA strand breaks. Addnl., the MutY enzyme was purified and its A-G-specific glycosylase activity determined

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=> E WELLER S/AU
=> S E3,E9,E14-E16
             18 "WELLER S"/AU
              2 "WELLER S K"/AU
             11 "WELLER SANDRA"/AU
             73 "WELLER SANDRA K"/AU
              1 "WELLER SANDRA KNOWLES"/AU
L26         105 ("WELLER S"/AU OR "WELLER S K"/AU OR "WELLER SANDRA"/AU OR "WELL
                ER SANDRA K"/AU OR "WELLER SANDRA KNOWLES"/AU)

=> E MYERS R/AU

=> S E3,E66,367
           9692 E3
             51 E66
           5335 367
L27           0 E3,E66,367
                (E3(W)E66(W)367)

=> S E3,E66,E67
             68 "MYERS R"/AU
              2 "MYERS RICH"/AU
             30 "MYERS RICHARD"/AU
L28         100 ("MYERS R"/AU OR "MYERS RICH"/AU OR "MYERS RICHARD"/AU)

=> E REUVEN N/AU
=> S E4-E6
              2 "REUVEN NINA B"/AU
              1 "REUVEN NINA BACHE"/AU
             14 "REUVEN NINA BACHER"/AU
L29          17 ("REUVEN NINA B"/AU OR "REUVEN NINA BACHE"/AU OR "REUVEN NINA
                BACHER"/AU)

=> S L26,L28,L29
L30         217 (L26 OR L28 OR L29)

=> S L30 AND L6
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L31 5 L30 AND L6

=> S L31 NOT L14
L32 2 L31 NOT L14

=> S L30 AND (L12,L13)
L33 19 L30 AND ((L12 OR L13))

=> S L33 NOT L14
L34 14 L33 NOT L14

=> S L32,L34
L35 16 (L32 OR L34)

=> D 1-16 CBIB ABS

L35 ANSWER 1 OF 16 CAPLUS COPYRIGHT 2005 ACS on STN
2003:1014110 Document No. 140:178077 The Rep protein of adeno-associated virus type 2 interacts with single-stranded DNA-binding proteins that enhance viral replication. Stracker, Travis H.; Cassell, Geoffrey D.; Ward, Peter; Loo, Yueh-ming; van Breukelen, Bas; Carrington-lawrence, Stacy D.; Hamatake, Robert K.; van der Vliet, Peter C.; Weller, Sandra K.; Melendy, Thomas; Weitzman, Matthew D. (Laboratory of Genetics, The Salk Institute for Biological Studies, La Jolla, CA, 92037, USA). Journal of Virology, 78(1), 441-453 (English) 2004. CODEN: JOVIAM. ISSN: 0022-538X. Publisher: American Society for Microbiology.
AB Adeno-associated virus (AAV) type 2 is a human parvovirus whose replication is dependent upon cellular proteins as well as functions supplied by helper viruses. The minimal herpes simplex virus type 1 (HSV-1) proteins that support AAV replication in cell culture are the helicase-primase complex of UL5, UL8, and UL52, together with the UL29 gene product ICP8. We show that AAV and HSV-1 replication proteins colocalize at discrete intranuclear sites. Transfections with mutant genes demonstrate that enzymic functions of the helicase-primase are not essential. The ICP8 protein alone enhances AAV replication in an in vitro assay. We also show localization of the cellular replication protein A (RPA) at AAV centers under a variety of conditions that support replication. In vitro assays demonstrate that the AAV Rep68 and Rep78 proteins interact with the single-stranded DNA-binding proteins (ssDBPs) of Ad (Ad-DBP), HSV-1 (ICP8), and the cell (RPA) and that these proteins enhance binding and nicking of Rep proteins at the origin. These results highlight the importance of intranuclear localization and suggest that Rep interaction with multiple ssDBPs allows AAV to replicate under a diverse set of conditions.

L35 ANSWER 2 OF 16 CAPLUS COPYRIGHT 2005 ACS on STN
2003:787687 Document No. 140:105847 The Role of DNA Recombination in Herpes Simplex Virus DNA Replication. Wilkinson, Dianna; Weller, Sandra (Department of Microbiology, University of Connecticut Health Center, Farmington, CT, 06030, USA). IUBMB Life, 55(8), 451-458 (English) 2003. CODEN: IULIF8. ISSN: 1521-6543. Publisher: Taylor & Francis Ltd..
AB A review. In many organisms the processes of DNA replication and recombination are closely linked. For instance, in bacterial and eukaryotic systems, replication forks can become stalled or damaged, in many cases leading to the formation of double stranded breaks. Replication restart is an essential mechanism in which the recombination and repair machinery can be used to continue replication after such a catastrophic event. DNA viruses of bacteria such as lambda and T4 also rely heavily on DNA recombination to replicate their genomes and both viruses encode specialized gene products which are required for recombination-dependent replication. In this review, we examine the linkage between replication and recombination in the eukaryotic pathogen, Herpes Simplex Virus Type 1 (HSV-1). The evidence that recombination plays an intrinsic role in HSV-1 DNA replication and the infection process will be reviewed. We have recently demonstrated that HSV-1 encodes two proteins which may be analogous to

the lambda phage recombination system, Redα and β. The HSV-1 alkaline nuclease, a 5' to 3' exonuclease, and ICP8, a single stranded DNA binding protein, can carry out strand annealing reactions similar to those carried out by the lambda Red system. In addition, evidence suggesting that host recombination proteins may also be important for HSV-1 replication will be reviewed. In summary, it is likely that HSV-1 infection will require both viral and cellular proteins which participate in various pathways of recombination and that recombination-dependent replication is essential for the efficient replication of viral genomes.

L35 ANSWER 3 OF 16 CAPLUS COPYRIGHT 2005 ACS on STN

2003:246814 Document No. 139:31625 Recruitment of polymerase to herpes simplex virus type 1 replication foci in cells expressing mutant primase (UL52) proteins. Carrington-Lawrence, Stacy D.; Weller, Sandra K. (Department of Microbiology, University of Connecticut Health Center, Farmington, CT, 06032-3205, USA). Journal of Virology, 77(7), 4237-4247 (English) 2003. CODEN: JOVIAM. ISSN: 0022-538X. Publisher: American Society for Microbiology.

AB The ordered assembly of the herpes simplex virus (HSV) type 1 replication apparatus leading to replication compartments likely involves the initial assembly of five viral replication proteins, ICP8, UL9, and the heterotrimeric helicase-primase complex (UL5-UL8-UL52), into replication foci. The polymerase and polymerase accessory protein are subsequently recruited to these foci. Four stages of viral infection (stages I to IV) have been described previously (J. Burkham, D. M. Coen, and S. K. Weller, J. Virol. 72:10100-10107, 1998). Of these, stage III foci are equivalent to the previously described promyelocytic leukemia protein (PML)-associated prereplicative sites and contain all seven replication proteins. A series of mutations were constructed in the putative primase subunit, UL52, of the helicase-primase and the mutant proteins analyzed for their abilities to form intermediates leading to the formation of replication compartments. The results shown in this paper are consistent with the model that the five proteins, ICP8, UL5, UL8, UL9, and UL52, form a scaffold and that formation of this scaffold does not rely on enzymic functions of the helicase and primase. Furthermore, recruitment of polymerase to this scaffold requires the presence of an active primase subunit. These results suggest that polymerase recruitment to replication foci requires primer synthesis. Furthermore, they support the existence of two types of stage III intermediates in the formation of replication compartments: stage IIIa foci, which form the scaffold, and stage IIIb foci, which contain, in addition, HSV polymerase, the polymerase accessory subunit, and cellular factors such as PML.

L35 ANSWER 4 OF 16 CAPLUS COPYRIGHT 2005 ACS on STN

2002:536279 Document No. 137:275441 The product of the UL12.5 gene of herpes simplex virus type 1 is not essential for lytic viral growth and is not specifically associated with capsids. Martinez, Rik; Goldstein, Joshua N.; Weller, Sandra K. (Department of Microbiology, University of Connecticut Health Center, Farmington, CT, 06030, USA). Virology, 298(2), 248-257 (English) 2002. CODEN: VIRLAX. ISSN: 0042-6822. Publisher: Elsevier Science.

AB The herpes simplex virus type 1 UL12 gene encodes a pH-dependent DNase termed alkaline nuclease. An N-terminally truncated version of the UL12 gene, called UL12.5, was shown to be translated independently from a subgenic mRNA which shares its 3' terminus with the full-length UL12 mRNA. We showed previously that the UL12.5 gene product cannot compensate for the absence of the full-length UL12 gene product (R. Martinez, L. Shao, J. C. Bronstein, P. C. Weber, and S. K. Weller, 1996, Virol. 215, 152-164); however, it was not known whether UL12.5 itself performs an essential function during lytic viral growth. In this article the initiation codon for the UL12.5 gene product was mapped and altered to create a gene no longer capable of producing UL12.5. This mutation was introduced into the viral genome to create a virus which was capable of producing full-length UL12 but not UL12 .5. The growth properties of this virus indicate that UL12.5 is not essential for viral growth in culture. UL12.5 was previously reported to

represent a capsid-associated form of alkaline nuclease (J. C. Bronstein, S. K. Weller, and P. C. Weber, 1997, J. Virol. 71, 3039-3047). Sucrose sedimentation anal. of capsids from cells infected with wild-type or mutant viruses indicates that both UL12 and UL12.5 are found in fractions from across the sucrose gradient which do not always correlate with the presence of viral capsids. Furthermore, UL12.5 is found in fractions across the gradient even in cells infected under conditions in which no capsids are formed. These results indicate that UL12.5 does not specifically associate with viral capsids. Taken together, these data indicate that UL12 .5 is not likely to play an important role in lytic viral infection.

L35 ANSWER 5 OF 16 CAPLUS COPYRIGHT 2005 ACS on STN
2001:167464 Document No. 135:254297 Growth and recombination of phage λ in the presence of exonuclease V from Bacillus subtilis. Stahl, F.; Bowers, R., Jr.; Mooney, D.; Myers, R.; Stahl, M.; Thomason, L. (Institute of Molecular Biology, University of Oregon, Eugene, OR, 97403-1229, USA). Molecular and General Genetics, 264(5), 716-723 (English) 2001. CODEN: MGGEAE. ISSN: 0026-8925. Publisher: Springer-Verlag.
AB When expressed in Escherichia coli, the AddAB exonuclease/ recombinase from Bacillus subtilis blocks the growth of phage λ. Mutants of λ that are deleted for ea47, a gene of unknown function which is expressed early in the lytic cycle, are not blocked for growth. The blocked-growth phenotype of λ ea47+ in the presence of AddAB is expressed only when phage DNA replication is permitted.

L35 ANSWER 6 OF 16 CAPLUS COPYRIGHT 2005 ACS on STN
1998:759364 Document No. 130:107425 ND10 protein PML is recruited to herpes simplex virus type 1 prereplicative sites and replication compartments in the presence of viral DNA polymerase. Burkham, Jennifer; Coen, Donald M.; Weller, Sandra K. (Dep. Microbiology, Univ. Connecticut Health Center, Farmington, CT, 06030, USA). Journal of Virology, 72(12), 10100-10107 (English) 1998. CODEN: JOVIAM. ISSN: 0022-538X. Publisher: American Society for Microbiology.
AB Herpes simplex virus type 1 (HSV-1) infection results in the disruption of ND10 (also called nuclear bodies, PODs, or PML-associated bodies), which are nuclear matrix domains of unknown function present in mammalian cells. After ND10 disruption, viral transcription and DNA replication occur in globular nuclear domains called replication compartments. In this report, 4 stages of infection are defined by using antibodies to ICP8 (also called SSB and UL29) and the ND10 antigen PML. Immediately after infection, cells contain intact ND10 as detected by staining for PMLs (stage I); within 1 h, however, ND10 are disrupted and cells begin to exhibit diffuse staining for the major viral DNA binding protein, ICP8 (stage II). After all ND10 have been disrupted, foci which resemble but are not equivalent to ND10 appear, containing both PML and ICP8 (stage III). Cells infected with mutants defective in the helicase-primase or origin binding protein are unable to form stage III foci. Cells infected with a mutant that is null for the polymerase catalytic subunit, however, form stage III-like ICP8 foci which do not contain PML. Thus, stage III foci recruit the cellular PML protein in the presence but not the absence of HSV polymerase. PML was recruited to stage III foci in some but not all cells infected with a mutant defective in the polymerase accessory protein, UL42. Thus, UL42 is not required for the recruitment of PML to viral foci. In wild-type infection, stage III cells are quickly replaced by cells containing replication compartments (stage IV). PML and ICP8 staining are both observed within replication compartments, indicating a potential role for PML in HSV-1 replication. Models for the role of ND10 proteins in the formation of replication compartments are discussed.

L35 ANSWER 7 OF 16 CAPLUS COPYRIGHT 2005 ACS on STN
1998:672178 Document No. 130:33889 In vitro processing of herpes simplex virus type 1 DNA replication intermediates by the viral alkaline nuclease,

UL12. Goldstein, Joshua N.; Weller, Sandra K. (Department of Microbiology, University of Connecticut Health Center, Farmington, CT, 06030, USA). Journal of Virology, 72(11), 8772-8781 (English) 1998. CODEN: JOVIAM. ISSN: 0022-538X. Publisher: American Society for Microbiology.

AB Herpes simplex virus type 1 (HSV-1) DNA replication intermediates exist in a complex nonlinear structure that does not migrate into a pulsed-field gel. Genetic evidence suggests that the product of the UL12 gene, termed alkaline nuclease, plays a role in processing replication intermediates. In this study we have tested the hypothesis that alkaline nuclease acts as a structure-specific resolvase. Cruciform structures generated with oligonucleotides were treated with purified alkaline nuclease; however, instead of being resolved into linear duplexes as would be expected of a resolvase activity, the artificial cruciforms were degraded. DNA replication intermediates were isolated from the well of a pulsed-field gel ("well DNA") and treated with purified HSV-1 alkaline nuclease. Although alkaline nuclease can degrade virion DNA to completion, digestion of well DNA results in a smaller-than-unit-length product that migrates as a heterogeneous smear; this product is resistant to further digestion by alkaline nuclease. The smaller-than-unit-length products are representative of the entire HSV genome, indicating that alkaline nuclease is not inhibited at specific sequences. To further probe the structure of replicating DNA, well DNA was treated with various known nucleases; our results indicate that replicating DNA apparently contains no accessible double-stranded ends but does contain nicks and gaps. Our data suggest that UL12 functions at nicks and gaps in replicating DNA to correctly repair or process the replicating genome into a form suitable for encapsidation.

L35 ANSWER 8 OF 16 CAPLUS COPYRIGHT 2005 ACS on STN

1998:648562 Document No. 130:2077 Functional conservations of the alkaline nuclease of herpes simplex type 1 and human cytomegalovirus. Gao, Min; Robertson, Barbara J.; McCann, Patrick J., III; O'Boyle, Donald R., II; Weller, Sandra K.; Newcomb, William W.; Brown, Jay C.; Weinheimer, Steven P. (Department of Virology, Bristol-Myers Squibb Pharmaceutical Research Institute, Wallingford, CT, 06492-7660, USA). Virology, 249(2), 460-470 (English) 1998. CODEN: VIRLAX. ISSN: 0042-6822. Publisher: Academic Press.

AB The herpes simplex virus type 1 UL 12 gene product, alkaline nuclease (AN), appears to be involved in viral DNA processing and capsid egress from the nucleus. Although the HSV-1 AN is not absolutely essential for viral replication in tissue culture, conservation of the AN gene in all herpesviruses suggests an important role in the life cycle of herpesviruses. The counterpart of HSV-1 AN for human cytomegalovirus (HCMV) is the UL98 gene product. To examine whether the HCMV AN could substitute for HSV-1 AN, the authors performed trans-complementation expts. using a HSV-1 amplicon plasmid carrying the HCMV UL98 gene. These results indicate (1) HCMV AN can complement the growth of the HSV-1 AN deletion mutant UL12lacZ virus in trans; (2) a new recombinant virus, UL12laZcUL98/99, appears to be generated by the integration of the HCMV UL98 gene into the HSV-1 UL12lacZ viral genome; and (3) in contrast to its parental HSV-1 UL12lacZ virus, capsids formed in UL12lacZUL98/99-infected Vero cells were able to transport from the nucleus to the cytoplasm and mature into infectious viruses. These results demonstrate a functional conservation of AN between HSV-1 and HCMV. (c) 1998 Academic Press.

L35 ANSWER 9 OF 16 CAPLUS COPYRIGHT 2005 ACS on STN

1998:312234 Document No. 129:51865 The exonuclease activity of HSV-1 UL12 is required for in vivo function. Goldstein, Joshua N.; Weller, Sandra K. (Department of Microbiology, University of Connecticut Health Center, Farmington, CT, 06030-3205, USA). Virology, 244(2), 442-457 (English) 1998. CODEN: VIRLAX. ISSN: 0042-6822. Publisher: Academic Press.

AB The herpes simplex virus type 1 (HSV-1) UL12 gene encodes an alkaline pH-dependent DNase termed alkaline nuclease. A recombinant UL12 knockout mutant, AN-1, is severely compromised for growth, and anal. of this mutant suggests that UL12 plays a role in processing complex DNA replication intermediates (R. Martinez, et al., 1996). This processing step may be required for the generation of capsids that are competent for egress from the nucleus to the cytoplasm. In this report, we address the question of whether the AN-1 growth phenotype is due to the loss of UL12 catalytic activity. We constructed two point mutations in a highly conserved region (motif II) of UL12 and purified wild-type and mutant enzymes from a baculovirus expression system. Both mutant proteins are stable, soluble, and competent for correct nuclear localization, suggesting that they have retained an intact global conformation. Neither mutant protein, however, exhibits exonuclease activity. In order to examine the in vivo effects of these mutations, we determined whether expression of mutant proteins from amplicon plasmids could complement AN-1. While the wild-type plasmid complements the growth of the null mutant, neither UL12 mutant can do so. Loss of exonuclease activity therefore correlates with loss of in vivo function.

L35 ANSWER 10 OF 16 CAPLUS COPYRIGHT 2005 ACS on STN
1998:113356 Document No. 128:228366 The herpes simplex virus type 1 cleavage/packaging protein, UL32, is involved in efficient localization of capsids to replication compartments. Lamberti, Carmela; Weller, Sandra K. (Department of Microbiology, University of Connecticut Health Center, Farmington, CT, 06030-3205, USA). Journal of Virology, 72(3), 2463-2473 (English) 1998. CODEN: JOVIAM. ISSN: 0022-538X. Publisher: American Society for Microbiology.

AB Six genes, including UL32, have been implicated in the cleavage and packaging of herpesvirus DNA into pre-assembled capsids. We have isolated a UL32 insertion mutant which is capable of near-wild-type levels of viral DNA synthesis; however, the mutant virus is unable to cleave and package viral DNA, consistent with the phenotype of a previously isolated temperature-sensitive herpes simplex virus type 1 mutant, tsN20 (P. A. Schaffer, G. M. Aron, N. Biswal, and M. Benyesh-Melnick, Virol. 52:57-71, 1973). A polyclonal antibody which recognizes UL32 was previously used by Chang et al. (Y. E. Chang, A. P. Poon, and B. Roizman, J. Virol. 70:3938-3946, 1996) to demonstrate that UL32 accumulates predominantly in the cytoplasm of infected cells. In this report, a functional epitope-tagged version of UL32 showed that while UL32 is predominantly cytoplasmic, some nuclear staining which colocalizes with the major DNA binding protein (ICP8, UL29) in replication compartments can be detected. We have also used a monoclonal antibody (5C) specific for the hexon form of major capsid protein VP5 to study the distribution of capsids during infection. In cells infected with wild-type KOS (6 and 8 h postinfection), 5C staining patterns indicate that capsids are present in nuclei within replication compartments. These results suggest that cleavage and packaging occur in replication compartments at least at 6 and 8 h postinfection. Cells infected with the UL32 mutant exhibit a hexon staining pattern which is more diffusely distributed throughout the nucleus and which is not restricted to replication compartments. We propose that UL32 may play a role in bringing preassembled capsids to the sites of DNA packaging and that the failure to localize to replication compartments may explain the cleavage/packaging defect exhibited by this mutant. These results suggest that the UL32 protein is required at a step distinct from those at which other cleavage and packaging proteins are required and may be involved in the correct localization of capsids within infected cells.

L35 ANSWER 11 OF 16 CAPLUS COPYRIGHT 2005 ACS on STN
1997:324713 Document No. 127:47621 Herpes simplex virus type 1 prereplicative sites are a heterogeneous population: only a subset are likely to be precursors to replication compartments. Lukonis, Christopher J.; Burkham, Jennifer; Weller, Sandra K. (Dep. of Microbiology, University of Connecticut Health Center, Farmington, CT, 06030, USA). Journal of Virology, 71(6), 4771-4781 (English) 1997. CODEN: JOVIAM.

ISSN: 0022-538X. Publisher: American Society for Microbiology.

AB When herpes simplex virus type 1 (HSV-1) DNA replication is blocked by viral polymerase inhibitors, such as phosphonoacetic acid (PAA) or acyclovir (ACV), UL29 (ICP8) localizes to numerous punctate nuclear foci which are called prereplicative sites. Since this pattern can form in cells infected with mutants which are defective in UL5, UL8, UL9, or UL52 in the presence of polymerase inhibitors, the authors previously proposed that it is unlikely that these numerous UL29 foci actually represent a functional subassembly of viral replication proteins that could lead to the formation of replication compartments. Here, the authors have investigated the requirement for formation of the prereplicative site pattern by using double mutants of HSV. From the anal. of mutants lacking both UL5 and UL9, it was concluded that neither viral helicase is required for the prereplicative site pattern to form as long as a polymerase inhibitor is present. From the anal. of mutants defective in both UL30 and UL5, we suggest that the prereplicative site pattern can form under conditions in which viral and/or cellular polymerases are inhibited. Furthermore, reexamn. of the UL29 staining pattern in cells infected with wild-type virus in the presence of PAA reveals that at least two different UL29 staining patterns can be detected in these cells. One population of cells contains numerous (greater than 20) punctate UL29 foci which are sites of cellular DNA synthesis. In another population of cells, fewer punctate foci (less than 15) are detected, and component of nuclear matrix structures known as ND10. It is proposed that ND10-associated UL29 sites represent domains at which replication compartments form.

L35 ANSWER 12 OF 16 CAPLUS COPYRIGHT 2005 ACS on STN

1997:185000 Document No. 126:274081 The product of the UL12.5 gene of herpes simplex virus type 1 is a capsid-associated nuclease. Bronstein, Joel C.; Weller, Sandra K.; Weber, Peter C. (Infect. Dis. Section, Parke-Davis Pharm. Res., Div. Warner-Lambert Co., Ann Arbor, MI, 48105, USA). Journal of Virology, 71(4), 3039-3047 (English) 1997. CODEN: JOVIAM. ISSN: 0022-538X. Publisher: American Society for Microbiology.

AB The UL12 open reading frame of herpes simplex virus type 1 (HSV-1) encodes a DNase that is frequently referred to as alkaline nuclease (AN) because of its high pH optimum. Recently, an alternate open reading frame designated UL12.5 was identified within the UL12 gene. UL12.5 and UL12 have the same translational stop codon, but the former utilizes an internal methionine codon of the latter gene to initiate translation of a 60-kDa amino-terminal truncated form of AN. Since the role of the UL12.5 protein in the HSV-1 life cycle has not yet been determined, its properties were investigated in this study. Unlike AN, which can be readily solubilized from infected cell lysates, the UL12.5 protein was found to be a highly insol. species, even when isolated by high-salt detergent lysis. Since many of the structural polypeptides which constitute the HSV-1 virion are similarly insol., a potential association of UL12.5 protein with virus particles was examined By using Western blot anal., the UL12 .5 protein could be readily detected in prepns. of intact virions, isolated capsid classes, and even capsids that had been extracted with 2 M guanidine-HCl. In contrast, AN was either missing or present at only low levels in each of these structures. Since the inherent insoly. of the UL12.5 protein prevented its potential DNase activity from being assayed in infected-cell lysates, partially purified fractions of soluble UL12.5 protein were generated by selectively solubilizing either insol. infected-cell proteins or isolated capsid proteins with urea and renaturing them by stepwise dialysis. Initial anal. of these prepns. revealed that they did contain an enzymic activity that was not present in comparable fractions from cells infected with a UL12.5 null mutant of HSV-1. Addnl. biochem. characterization revealed that UL12.5 protein was similar to AN with respect to pH optimum, ionic strength, and divalent cation requirements and possessed both exonucleolytic and endonucleolytic functions. The finding that the UL12.5 protein represents a capsid-associated form of AN which exhibits nucleolytic activity suggests that it may play some role in the processing of genomic DNA during encapsidation.

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1996:629315 Document No. 125:270022 Intracellular localization of the herpes simplex virus type-1 origin binding protein, UL9. Malik, Ajay K.; Shao, Lei; Shanley, John D.; Weller, Sandra K. (Departments Microbiology, University Connecticut Health Center, Farmington, CT, 06030, USA). Virology, 224(2), 380-389 (English) 1996. CODEN: VIRLAX. ISSN: 0042-6822. Publisher: Academic.

AB UL9 is the origin binding protein of herpes simplex virus type-1 (HSV-1). A UL9-specific monoclonal antibody (17B) whose epitope maps to the N-terminal 33 amino acids was used to study the localization of UL9 in infected and transfected cells. We demonstrate the colocalization of UL9 and the HSV-1 single-strand DNA binding protein (ICP8 or UL29) in replication compartments, sits of viral DNA synthesis. On the other hand, UL9 does not completely colocalize with ICP8 in prereplicative sites, structures observed under conditions that inhibit viral DNA polymerase. Cells transfected with various deletion or pyruvate kinase fusion constructs were analyzed by indirect immunofluorescence assay to define the nuclear localization signal (NLS) of UL9. Deletion anal. showed that the region required for nuclear localization lies within the C-terminal DNA binding domain (amino acids 535-851). Various regions of UL9 were tested in fusion constructs for their ability to direct the normally cytoplasmic chicken pyruvate kinase protein to the nucleus. A fusion construct containing the carboxy-terminal 107 residues (amino acids 745-851) localized efficiently to the nucleus, whereas a fusion construct containing the N-terminal 660 amino acids of UL9 was unable to do so. Mutations designed to alter a potential NLS sequence (793-KREFAGARFKLR-804) within the C-terminal 107 residues result in a mutant UL9 protein which fails to localize efficiently to the nucleus. These results suggest that the major NLS of UL9 maps within the C-terminal 107 amino acids.

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1996:69681 Document No. 124:112225 The product of a 1.9-kb mRNA which overlaps the HSV-1 alkaline nuclease gene (UL12) cannot relieve the growth defects of a null mutant. Martinez, Rik; Shao, Lei; Bronstein, Joel C.; Weber, Peter C.; Weller, Sandra K. (Dept. Microbiol., Univ. Connecticut Health Center, Farmington, CT, 06030, USA). Virology, 215(2), 152-64 (English) 1996. CODEN: VIRLAX. ISSN: 0042-6822. Publisher: Academic.

AB Alkaline nuclease, a relatively abundant viral phosphoprotein in herpes simplex virus type 1 (HSV-1)- or HSV-2-infected cells, is encoded by a 2.3-kb mRNA (R. H. Costa, K. G. Draper, L. Banks, K. L. Powell, G. Cohen, R. Eisenberg, and E. K. Wagner, 1983, J. Virol. 48, 591-603). This mRNA is a member of a family of five unspliced 3'-coterminal messages. Costa et al. (1983), proposed that another member of this family of mRNAs (1.9-kb) may encode an N-terminally truncated protein which shares its carboxy-terminus with the alkaline nuclease protein. We previously described the isolation of AN-1, a deletion/insertion mutant of the alkaline nuclease gene (S. K. Weller, R. M. Seghatoleslami, L. Shao, D. Rowse, and E. P. Carmichael, 1990, J. Gen. Virol. 71, 2941-2952). The deletion in AN-1 would be predicted to abolish gene products of both the 2.3- and the 1.9-kb mRNAs. To investigate whether the putative truncated version of alkaline nuclease encoded by the 1.9-kb mRNA has enzymic activity and plays a role in the viral life cycle, a viral mutant (AN-F1) was constructed which is predicted to abolish the gene product of the 203-kb mRNA (full-length alkaline nuclease) but leave intact the putative product of the 1.9-kb mRNA. Using a highly sensitive polyclonal antiserum raised against a bacterially expressed full-length alkaline nuclease, we observed a 60-kDa protein in KOS- and AN-F1-infected cells but not in AN-1-infected cells. This suggests that the 60-kDa protein is likely to be expressed from the 1.9-kb mRNA; the open reaching frame is now designated UL 12.5. Despite the presence of the 60-kDa band, AN-F1 failed to exhibit any alkaline exonuclease activity. This result suggests that the truncated polypeptide (UL 12.5) is not enzymically active, has low levels of activity, or possesses enzymic activity which is not detected because of the low abundance of

the polypeptide. AN-1 and AN-F1 are both severely restricted with respect to growth in Vero cells, as viral yields are 100- to 1000-fold lower than those of wild-type virus. We previously reported that the major defect in AN-1 is in the ability of DNA-containing capsids which form in the nucleus to mature into the cytoplasm (L. Shao, L. M. Rapp, and S. K. Weller, 1993, Virol. 196, 146-162); AN-F1 exhibits the same defect. These results indicate that although the 1.9-kb mRNA encodes a 60-kDa protein presumably from the UL 12.5 open reading frame, this polypeptide cannot substitute for the full-length UL12 product.

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1995:909873 Document No. 123:330878 Old and new concepts for the role of chi in bacterial recombination. Stahl, F.; Myers, R. (Institute of Molecular Biology, University of Oregon, Eugene, OR, 97403-1229, USA). Journal of Heredity, 86(5), 327-9 (English) 1995. CODEN: JOHEA8. ISSN: 0022-1503. Publisher: Oxford University Press.

AB A review with 47 refs. The DNA sequence 5'[GCTGGTGG]3', which is called χ, stimulates recombination that is mediated by the RecBCD pathway of Escherichia coli. In 1981, a model was proposed in which the RecBCD enzyme enters DNA at a double-chain end. The enzyme then travels between the chains by unwinding and rewinding the DNA at different rates so that the traveling enzyme becomes encumbered by a region of unwound DNA. Upon meeting χ, the enzyme was supposed to cut one of the two unwound chains, generating thereby a recombinagenic single-chain end. The model, based on microscopical observations of RecBCD enzyme interacting with linear duplex DNA, was supported by the subsequent finding that RecBCD acting in vitro under certain conditions did deliver a nick at χ. This widely embraced model has been challenged by a model in which the exonuclease activity of RecBCD destroys DNA from the enzyme's entry site to χ. The role of χ according to the new model is to inhibit this nuclease activity of RecBCD, perhaps by ejecting the RecD subunit from the enzyme, thereby revealing the enzyme's recombinase activity.

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1991:75971 Document No. 114:75971 The herpes simplex virus type 1 alkaline nuclease is not essential for viral DNA synthesis: isolation and characterization of a lacZ insertion mutant. Weller, Sandra K.; Seghatoleslami, M. Reza; Shao, Lei; Rowse, Debra; Carmichael, Ellen P. (Health Cent., Univ. Connecticut, Farmington, CT, 06030, USA). Journal of General Virology, 71(12), 2941-52 (English) 1990. CODEN: JGVIAY. ISSN: 0022-1317.

AB Herpes simplex virus type 1 (HSV-1) encodes a novel enzyme activity, the alkaline nuclease, whose precise role in the viral replication cycle remains obscure. The alkaline nuclease gene corresponds to the UL12 open reading frame, which is predicted to encode a protein of 626 amino acid residues. The isolation and characterization of a null mutant of the gene for the viral alkaline nuclease is described in which 917 bp from the N-terminal half of the gene (corresponding to residues 70 to 375) were deleted and replaced by the insertional mutagen ICP6::lacZ. The resulting mutant virus, AN-1, was propagated in helper cells (S22) which express the wild-type version of the alkaline nuclease gene. Mutant AN-1 growth in Vero cells is severely restricted, although small amts. of infectious virus are produced. On the other hand, wild-type levels of viral DNA and late viral proteins are expressed in virus AN-1-infected Vero cells. These results indicate that the HSV-1 alkaline nuclease gene product is not essential for viral DNA synthesis but may play a role in the processing or packaging of viral DNA into infectious virions. Possible roles in the viral infectious cycle are discussed.

	L #	Hits	Search Text	DBs
1	L1	5194	RECOMBINASE	US-PGPUB; USPAT
2	L2	24878	HERPES SIMPLEX	US-PGPUB; USPAT
3	L3	391	UL12 OR (UL ADJ "12")	US-PGPUB; USPAT
4	L4	172	ICP8 OR (iCP ADJ "8")	US-PGPUB; USPAT
5	L5	3	L3 AND L4	US-PGPUB; USPAT
6	L7	7953	DNA ADJ BINDING ADJ (POLYPEPTIDE OR PROTEIN)	US-PGPUB; USPAT
7	L8	1	L6 AND L7	US-PGPUB; USPAT
8	L6	5	ALKALINE NUCLEASE	US-PGPUB; USPAT